IN THE APPLICATION:

Please amend page 9 paragraph 5:

Figure 1, 1A-1D. Complete cDNA sequence of FtsZ-mt2 from *Phytophthora infestans*, showing nucleotide sequence (SEQ ID NO:9) and predicted amino acid sequence (SEQ IDN O:10).

Please amend page 9, paragraph 6- page 10, paragraph 1:

Figure 2, 2A-2D. Alignment of FtsZ sequences from *Agrobacterium tumefaciens* (SEQ ID NO:11), *Sinorhizobium meliloti* (SEQ ID NO:12), *Bartonella clarridgeiae* (SEQ ID NO:13), *Rickettsia prowazekii* (SEQ ID NO:14), *Caulobacter crescentus* (SEQ ID NO:15), *Cyanidioschyzon merolae*-mt (SEQ ID NO:16), *Phytophthora infestans*-mt2 (SEQ ID NO:4), *Mallomonas splendens*-mt (SEQ ID NO:17), *Phytophthora infestans*-mt1 (SEQ ID NO:2), *Gentiana lutea*-cp (SEQ ID NO:18), *Nicotiana tabacum*-cp2-1 (SEQ ID NO:19), *Arabidopsis thaliana*-cp2 (SEQ ID NO:20), *Physcomitrella patens*-cp1 (SEQ ID NO:21), *Physcomitrella patens*-cp2 (SEQ ID NO:22), *Guillardia theta*-cp (SEQ ID NO:23), *Mallomonas splendens*-cp (SEQ ID NO:24), *Anabaena* (SEQ ID NO:25), *Synechocystis* (SEQ ID NO:26), *Arabidopsis thaliana*-cp1 (SEQ ID NO:27), *Pisum sativum*-cp (SEQ ID NO:28), *Nicotiana tabacum*-cp1-3 (SEQ ID NO:29), *Nicotiana tabacum*-cp1 (SEQ ID NO:30), *Nicotiana tabacum*-cp1-1 (SEQ ID NO:31), *and Nicotiana tabacum*-cp2 (SEQ ID NO:32).

Please amend page 25, paragraph 4- page 26, paragraph 1:

Potential targeting sites may be determined empirically and by any means known in the art. One strategy is to pinpoint sites which differ between oomycete mitochondrial forms of FtsZ and higher plant chloroplast forms of FtsZ. ~~Figure 2~~ Figures 2, 2A-2D shows a comparison of the FtsZ-mt1 and FtsZ-mt2 protein sequences with other known FtsZ proteins. Differences between clusters of similar sequences can be deterimined by comparison of sequence alignments. Potential targeting sites are found at the following positions in the protein sequenc: amino acid position 18, 30, 31, 62, 135, 142, 156-157, 159, 163, 189-190, 198, 210, 217, 223, 227, 236, 245, 251-252, 266, 271, 276, 287-289, 300, 302, and 306 (~~Figure 2~~Figures 2, 2A-2D). These sites show differences in FtsZ protein sequences between the cluster for mitochondria from lower eukaryoltes and an α-proteobacteria, and the cluster for higher plant chloroplasts and cyanobacteria.

Consequently, these sites represent embodiments for targeting with potntial inhibitors of FtsZ-mt function.

Please amend paragraph 2, on page 31:

~~Figure 2~~ Figures 2, 2A-2D shows a comparison of the FtsZ-mt1 and FtsZ-mt2 protein sequences with other known FtsZ proteins. Potential targeting sites are found at the following positions in the protein sequenc: amino acid position 18, 30, 31, 62, 135, 142, 156-157, 159, 163, 189-190, 198, 210, 217, 223, 227, 236, 245, 251-252, 266, 271, 276, 287-289, 300, 302, and 306. The indicated sites were well-clustered by homology with FtsZs from an (α)-proteobacteria and other mitochondrial forms, but well-separated from the cluster for the chloroplast forms and cyanobacterial FtsZs. Chemicals will be designed that can discriminate and recognize one of the amino acids in a given cluster. Such chemicals will only kill primitive eukaryotes having FtsZ-mt proteins, such as oomycetes, and some bacteria that have highly homologous FtsZ proteins, such as an α-proteobacterium, but will not affect other eukaryotes, including plants and animals.